

P65#26 -> Genes

DNA sequence 1665 b.p. gaattcgggttc ... caagccgaattc linear

PGO-1

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1 gaattcgggttcac ATG GCG GCT AAA GAC GTA AAA TTC GGT AAC GAC GCT CGT GTG AAA ATG CTG CGC GGC GTA AAC 77
1 M A A K D V K F G N D A R V K M L R G V N 21

78 GTA CTG GCA GAT GCA GTG AAA GTT ACC CTC GGC CCA AAA GGC CGT AAC GTA GTT CTG GAT AAA TCT TTC GGT GCA 152
22 V L A D A V K V T L G P K G R N V V L D K S F G A 46

153 CCG ACC ATC ACT AAA GAT GGT GTT TCC GTA GCA CGT GAA ATC GAA CTG GAA GAC AAG TTC GAA AAC ATG GGT GCG 227
47 P T I T K D G V S V A R E I E L E D K F E N M G A 71

228 CAG ATG GTG AAA GAA GTT GCC TCT AAA GCG AAC GAC GCT GCA GGT GAC GGT ACC ACC ACC GCA ACC GTA CTG GCT 302
72 Q M V K E V A S K A N D A A G D G T T T A T V L A 96

303 CAG TCC ATC ATC ACT GAA GGC CTG AAA GCC GTT GCT GCG GGC ATG AAC CCG ATG GAT CTG AAA CGT GGT ATC GAC 377
97 Q S I I T E G L K A V A A G M N P M D L K R G I D 121

378 AAA GCT GTC GCT GCT GCT GTT GAA GAA CTG AAA GCA CTG TCC GTA CCG TGC TCC GAC TCT AAA GCT ATT GCT CAG 452
122 K A V A A A V E E L K A L S V P C S D S K A I A Q 146

453 GTT GGT ACC ATC TCC GCT AAC TCC GAC GAA ACC GTA GGT AAA CTG ATC GCT GAA GCG ATG GAC AAA GTC GGT AAA 527
147 V G T I S A N S D E T V G K L I A E A M D K V G K 171

528 GAA GGC GTG ATC ACC GTT GAA GAC GGT ACC GGT CTG CAG GAC GAA CTG GAC GTG GTT GAA GGT ATG CAG TTC GAC 602
172 E G V I T V E D G T G L Q D E L D V V E G M Q F D 196

603 CGT GGC TAC CTG TCT CCT TAC TTC ATC AAC AAG CCG GAA ACT GGC GCA GTA GAA TTG GAA AGC CCG TTC ATC CTG 677
197 R G Y L S P Y F I N K P E T G A V E L E S P F I L 221

678 CTG GCT GAC AAG AAA ATC TCC AAC ATC CCG GAA ATG CTG CCG GTT CTG GAA GGT GTA GCG AAA GCA GGC AAA CCG 752
222 L A D K K I S N I R E M L P V L E A V A K A G K P 246

753 CTG CTG ATC ATC GCT GAA GAT GTT GAA GGC GAA GCG CTG GCA ACT CTG GTT GTT AAC ACC ATG CCG GGT ATC GTA 827
247 L I I A E D V E G E A L A T L V V N T M R G I V 271

828 AAA GTC GCT GCG GTT AAA GCA CCG GGC TTC GGC GAT CGT CGT AAA GCA ATG CTG CAG GAT ATC GCT ACC CTG ACC 902
272 K V A A V K A P G F G D R R K A M L Q D I A T L T 296

903 GGT GGT ACC GTT ATC TCT GAA GAG ATC GGT ATG GAG CTG GAA AAA GCA ACT CTG GAA GAT CTG GGC CAG GCG AAA 977
297 G G T V I S E E I G M E L E K A T L E D L Q A K 321

978 CCG GTT GTT ATC AAC AAA GAT ACC ACC ACC ATC ATC GAT GGC GTG GGC GAC GAA GCT GCA ATC CAG GGT CCG GTG 1052
322 R V V I N K D T T T I I D G V G D E A A I Q G R V 346

1053 ACT CAG ATT CGT CAG CAG ATC GAA GAA GCA ACT TCC GAC TAT GAC CGT GAA AAA CTG CAG GAG CCG GTA GCG AAA 1127
347 T Q I R Q Q I E E A T S D Y D R E K L Q E R V A K 371

1128 CTG GCA GGC GCG GTT GCG GTT ATC AAA GTT GGT GCT GCG ACT GAA GTT GAA ATG AAA GAG AAG AAA GCC CCG GTT 1202
372 L A G G V A V I K V G A A T E V E M K E K K A R V 396

1203 AAA GAT GCG CTG CAC GCT ACC CGT GCT GCG GTA GAA GAA GGC GTG GTT GCT GGT GGT GCG GTT ATT CCG 1277
397 S D A L H A T R A A V E E G V V A G G V A L I R 421

1278 GTA GCG TCT AAA ATT GCG GCG CTG AAA GGT CAG AAC GAA GAC CAG AAC GTA GGT ATC AAA GTT GCG CTG CCG GCA 1352
422 V A S K I A G L K G Q N E D Q N V G I K V A L R A 446

1353 ATG GAA TCC CCA CTG CGT CAA ATC GTA CTG AAC TGC GGC GAA GAG CCG TCT GTA GTG GCT AAC ACC GTG AAA GCC 1427
447 M E S P L R Q I V L N C G E E P S V V A N T V K A 471

1428 GGT GAC GGT AAC TAC GGT TAC AAC GGT GCA ACT GAA GAA TAC GGC AAC ATG ATC GAC ATG GGT ATC CTG GAT CCA 1502
472 G D G N Y G Y N A A T E E Y G N M I D M G I L P 496

1503 ACC AAA GTA ACT CGT TCT GCT CTG CAG TAC GCG GCT TCT GTT GCG GGT CTG ATG ATC ACC ACC GAG TGC ATG GTT 1577
497 T K V T R S A L Q Y A A S V A G L M I T T E C M V 521

1578 ACC GAC CTG CCG AAA GGC GAT GCA CCG GAC TGA GGT GCT GCT GGT GGT ATG GGC GGC ATG GGC GGA ATG ATG TGA 1652
522 T D L P K G D A P D L G A A G G M G G M G G M M 546

1653 caagccgaattc 1665

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Figure 1

P65#44 -> Genes

DNA sequence 1654 b.p. gaattcggttc ... aaagccgaattc linear

use to subclone for expression

P60-2

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1 gaattcggttcac ATG GCA AAA GAA ATT AAA TTT TCA TCA GAT GCC CGT TCA GCT ATG GTC CGT GGT GTC GAT ATC 77
1 M A K A I A S S D A R S A M V R G V D I 21

78 CTT GCA GAT ACT GTT AAA GTA ACT TTG GGA CCA AAA GGT CGC AAT GTC GTT CTT GAA AAG TCA TTC GGT TCA CCC 152
22 L A D T V K V T L G P K G R N V V L E K S F G S P 46

153 TTG ATT ACC AAT GAC GGT GTG ACT ATT GCC AAA GAA ATT GAA TTA GAA GAC CAT TTT GAA AAT ATG GGT GCC AAA 227
47 L I T N D G V T I A K E I E L E D H F E N M G A K 71

228 TTG GTA TCA GAA GTA GCT TCA AAA ACC AAT GAT ATC GCA GGT GAT GGA ACT ACA ACT GCA ACT GTT TTG ACC CAA 302
72 L V S E V A S K T N D I A G D G T T A T V L T Q 96

303 GCA ATC GTC CGT GAA GGA ATC AAA AAC GTC ACA GCA GGT GCA AAT CCA ATC GGT ATT CGT CGT GGG ATT GAA ACA 377
97 A I V R E G I K N V T A G A N P I G I R R G I E T 121

378 GCA GTT GCC GCA GCA GTT GAA GCT TTG AAA AAC AAC GTC ATC CCT GTT GCC AAT AAA GAA GCT ATC GCT CAA GTT 452
122 A V A A A V E A L K N N V I P V A N K E A I A Q V 146

453 GCA GCC GTA TCT TCT CGT TCT GAA AAA GTT GGT GAG TAC ATC TCT GAA GCA ATG GAA AAA GTT GGC AAA GAC GGT 527
147 A A V S S R S E K V G E Y I S E A M E K V G K D G 171

528 GTC ATC ACC ATC GAA GAG TCA CGT GGT ATG GAA ACA GAG CTT GAA GTC GTA GAA ATG CAG TTT GAC CGT GGT 602
172 V I T I E E S R G M E T E L E V V E G M Q F D R G 196

603 TAC CTT TCA CAG TAC ATG GTG ACA GAT AGC GAA AAA ATG GTG GCT GAC CTT GAA AAT CCG TAC ATT TTG ATT ACA 677
197 Y L S Q Y M V T D S E K M V A D L E N P Y I L I T 221

678 GAC AAG AAA ATT TCC AAT ATC CAA GAA ATC TTG CCA CTT TTG GAA AGC ATT CTC CAA AGC AAT CGT CCA CTC TTG 752
222 D K K I S N I Q E I L P L L E S I L Q S N R P L L 246

753 ATT ATT GCG GAT GAT GTG GAT GGT GAG GCT CTT CCA ACT CTT GTT TTG AAC AAG ATT CGT GGA ACC TTC AAC GTA 827
247 I I A D D V D G E A L P T L V L N K I R G T F N V 271

828 GTA GCA GTC AAG GCA CTT GGT TTT GGT GAC CGT CGC AAA GCC ATG CTT GAA GAT ATC GCC ATC TTA ACA GGC GGA 902
272 V A V K A P G F G D R R K A M L E D I A I L T G G 296

903 ACA GTT ATC ACA GAA GAC CTT GGT CTT GAG TTG AAA GAT GCG ACA ATT GAA GCT CTT GGT CAA GCA GCG AGA GTG 977
297 T V I T E D L G L E L K D A T I E A L G Q A A R V 321

978 ACC GTG GAC AAA GAT AGC ACG GTT ATT GTA GAA GGT GCA GGA AAT CCT GAA GCG ATT TCT CAC CGT GTT GCG GTT 1052
322 T V D K D S T V I V E G A G N P E A I S H R V A V 346

1053 ATC AAG TCT CAA ATC GAA ACT ACA ACT TCT GAA TTT GAC CGT GAA AAA TTG CAA GAA CGC TTG GCC AAA TTG TCA 1127
347 K S Q I E T T T S E F D R E K L Q E R L A K L S 371

1128 GGT GGT GTA GCG GTT ATT AAG GTC GGA GCC GCA ACT GAA ACT GAG TTG AAA GAA ATG AAA CTC CGC ATT GAA GAT 1202
372 G G V A V I K V G A A T E T E L K E M K L R I E D 396

1203 GCC CTC AAC GGT ACT CGT GCA GGT GTT GAA GAA GGT ATT GTT GCA GGT GGT GGA ACA GCT CTT GCC AAT GTG ATT 1277
397 A L N A T R A A V E E G I V A G G G T A L A N V I 421

1278 CCA GCT GTT GCT ACC TTG GAA TTG ACA GGA GAT GAA GCA ACA GGA CGT AAT ATT GTT CTC CGT GCT TTG GAA GAA 1352
422 A V A T L E L T G D E A T G R N I V L R A L E E 446

1353 GGT GTT CCA ATT GCT CAC AAT GCA GGA TTT GAA GGA TCT ATC GAT GTT ATC GAT CGT TTG AAA AAT GCT GAG CTT 1427
447 P V R Q I A H N A G F E G S I V I D R L K N A E L 471

1428 GGT ATA GGA TTC AAC GCA GCA ACT GGC GAG TGG GTT AAC ATG ATT GAT CAA GGT ATC ATT GAT CCA GTT AAA GTG 1502
472 G I G F N A A T G E W V N M I D Q G I I D P V K V 496

1503 AGT CGT TCA GCC GTA CAA AAT GCA GCA TCT GTA GCC AGC TTG ATT TTG ACA ACA GAA GCA GTC GTA GCC AAT AAA 1577
497 S R S A L Q N A A S V A S L I L T T E A V V A N K 521

1578 CCA GAA CCA GTA GCC CCA GCT CCA GCA ATG GAT CCA AGT ATG ATG GGT GGA ATG GGC GGA TGA aaagccgaattc 1654
522 P E P V A P A P A M D P S M H G G M G G 542

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Figure 2

Y65#5 -> Genes

DNA sequence 1662 b.p. gaattcggtttc ... caagcgaattc linear

Y60-1

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1 gaattcggtttc ATG GCG GCT AAA GAT GTA AAA TTC GGT AAC GAC GCT GGT GTA AAA ATG CTC CGC GGC GTA AAC 77
1 M A A K D V K F G N D A R V K M L R G V N 21

78 GTA CTG GCA GAC GCA GTT AAA GTA ACC CTG GCG CCG AAA GGC CGT AAC GTA GTG CTG GAC AAA TCC TTC GGC GCG 152
22 V L A D A Y K V T L G P K G R N V V L D K S F G A 46

153 CCA ACC ATC ACG AAA GAT GGT GTT TCT GTA GCA CGT GAA ATC GAG CTG GAA GAC AAG TTC GAA AAC ATG GGC GCG 227
47 P T I T K D G V S V A R E I E L E D K F E N M G A 71

228 CAG ATG GTG AAA GAA GTG GCC TCT AAA GCG AAC GAC GCT GCA GGC GAC GGT ACC ACC ACC GCG ACC GTG CTG GCT 302
72 Q M V K E V A S K A N D A A G D G T T A T V L A 96

303 CAG GCT ATC ATC ACC GAA GGT CTG AAA GCC GTT GCT GCG GGC ATG AAC CCA ATG GAT CTG AAA CGT GGT ATC GAC 377
97 Q A I I T E G L K A V A A G M N P M D L K R G I D 121

378 AAA GCT GTC GCG TCC GCT GTT GAA GAA CTG AAA GCG CTG TCC GTA CCG TGC TCT GAC TCT AAA GCC ATT GCT CAG 452
122 K A V A S A V E E L K A L S V P C S D S K A I A Q 146

453 GTA GGT ACC ATC TCC GCT AAC TCC GAC GAA ACC GTA GGT AAA CTG ATC GCG GAA GCG ATG GAT AAA GTC GGT AAA 527
147 V G G T I S A N S D E T V G K L I A E A M D K V G K 171

528 GAA GGC GTG ATC ACC GTT GAA GAC GGT ACC GGT GGT GAA GAA GAA CTG GAC GTG GTT GAA GGT ATG CAG TTC GAC 602
172 E G V I T V E D G T G L E D E L D V V E G M Q F D 196

603 CGC GGT TAC CTG TCC CCA TAC TTC ATC AAC AAG CCA GAA ACT GGC GCT GTT GAG CTG GAA AGC CCG TTC ATC CTG 677
197 R G Y L S P Y F I N K P E T G A V E L E S P F I L 221

678 CTG GCT GAC AAG AAA ATC TCC AAC ATC GCG GAA ATG CTG CCA GTG CTG GAA GCC GTT GCG AAA GCA GGC AAA CCG 752
222 L A D K K I S N I R E M L P V L E X V A K A G K P 246

753 CTG GTT ATC ATT GCT GAA GAC GTT GAA GCG GAA GCG CTG GCG ACC CTG GTG GTT AAC ACC ATG CGT GGC ATC GTG 827
247 L V I I A E D V E G E A L A T L V V N T M R G I V 271

828 AAA GTG GCT GCG GTT AAA GCA CCT GCG TTC GCG GAC CCG CGT AAA GCG ATG CTG CAG GAT ATC GCT ACC CTG ACC 902
272 K V A A V K A P G F G D R R K A M L Q D I A T L T 296

903 GGC GGT ACC GTC ATC TCT GAA GAG ATC GGT ATG GAG CTG GAA AAA GCG ACC CTG GAA GAC CTG GCG CAG GCT AAA 977
297 G G T V I S E E I G M E L E K A T L E D L G Q A K 321

978 CGT GTT GTG ATC AAC AAA GAC ACC ACC ACC ATC ATC GAT GGC GTG GGC GAC GAA GCG GCG ATT CAG GCG CGT GTT 1052
322 R V V I N K D T T T I I D G V G D E A A I Q G R V 346

1053 GGT CAG ATC CGT AAG CAG ATC GAA GAA GCC ACT TCC GAT TAC GAC CGT GAA AAA CTG CAG GAG CCG GTA GCG AAA 1127
347 G Q I R K Q I E E A T S D Y D R E K L Q E R V A K 371

1128 CTG GCA GGC GGT GTT GCG GTA ATC AAA GTC GGT GCT GCG ACT GAA GTT GAA ATG AAA GAG AAA AAA GCA CCG GTT 1202
372 L A G G V A V I K V G A A T E V E M K E K K A R V 396

1203 GAC GAT GCC CTG CAC GCG ACC CGT GCT GCG GTA GAA GAA GCG GTG GTT GCT GGT GGT GTG GCG CTG GTG CGT 1277
397 D D A L H A T R A A V E E G V V A G G G V A L V R 421

1278 GTT GCC GCG AAA CTG TCC GCG CTG ACT GCT CAG AAC GAA GAT CAG AAC GTG GGT ATC AAA GTT GCG CTG CCG GCA 1352
422 V A A K L S G L T A Q N E D Q N V G I K V A L R A 446

1353 ATG GAA GCT CCA CTG CGT CAG ATC GTG TCC AAC GCC GGT GAA GAG CCA TCT GTT GTG ACC AAC AAC GTG AAA GCA 1427
447 M E A P L R Q I V S N A G E E P S V V T N N V K A 471

1428 GGC GAA GGT AAC TAC GGT TAC AAC GCA GCA ACT GAA GAA TAC GGC AAC ATG ATC GAC TTC GGT ATC CTG GAT CCA 1502
472 G E G N Y G Y N A A T E E Y G N M I D F G I L D P 496

1503 ACC AAA GTG ACC CGT TCT GCT CTG CAG TAC GCG GCA TCT GTC GCT GCG CTG ATG ATC ACC ACC GAG TGC ATG GTG 1577
497 T K V T R S A L Q Y A A S V A G L M I T T E C M V 521

1578 ACC GAC CTG CTT AAA GCG GAC GCA CTT GAC TTA GGT GCT GCA GCG ATG GGT GCG ATG GCG GGT ATG ATG TGA caaa 1653
522 T D L P K G D A P D L G A A G M G G M G G M A 545

1654 gcggaattc 1662

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Figure 3

Y65#21 -> Genes

DNA sequence 1661 b.p. gaattcgggttc ... TAAGccgaattc linear

V261 - same in clone Y65#24, too
used to subclone for expression !!!

Y60-2

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1 gaattcgggttcgag atg gca aaa gaa atc aaa ttt tca gca gat ggc ggt gct gcc atg gtg cgc gga gtt gat atg 77
1 M A K E L R F S A D A R A A M V R G V D M 21

78 tta gca gat acc gtc aaa gta acg ctt ggt cct aaa ggc ggc aat gtt gtt ctt gaa aaa gct ttt ggt tct ccc 152
22 L A D T V K V T L G P K G R N V V L E K A F G S P 46

153 tta att act aat gac ggc gta acc att gct aaa gag atc gaa tta gaa gat cat ttt gaa aac atg gga gca aaa 227
47 L I T N D G V T I A K E I E L E D H F E N M G A K 71

228 ttg gtg tct gaa gtg gct tct aaa acc aat gat att gct ggt gat ggc acc act act gca aca gtt ttg aca caa 302
72 L V S E V A S K T N D I A G D G T T T A T V L T Q 96

303 gcc att gtt cat gaa gga cta aaa aat gtg aca gca ggt gct aat cca att ggt atc cgt cga ggc att gaa aca 377
97 A I V H E G L K N V T A G A N P I G I R R G I E T 121

378 gca aca gca aca gct gtt gaa gcc ttg aaa gcc att gct cca cct gta tct ggc aag gaa gct att gct cag gtc 452
122 A T A T A V E A L K A I A Q P V S G K E A I A Q V 146

453 gct gca gta tca tca cgc tct gaa aaa gtt gga gag tat atc tca gaa gct atg gag cgt gtg ggc aac gat ggt 527
147 A A V S S R S E K V G E Y I S E A M E R V G N D G 171

528 gtg att acc atc gaa gaa tct cga ggt atg gaa aca gaa ctt gaa gtg gtt gaa ggc atg caa ttt gac cgt ggt 602
172 V I T I E E S R G M E T E L E V V E G M Q F D R G 196

603 tac ctg tct caa tac atg gtc aca gac aat gaa aaa atg gtt gca gac ctt gaa aac cca ttt atc tta atc acc 677
197 Y L S Q Y M V T D N E K M V A D L E N P F I L I T 221

678 gat aaa aaa gtg tca aac atc caa gac att ttg cca cta ctt gag gaa gtt ctt aaa acc aac cgt cca tta ctc 752
222 D K K V S N I Q D I L P L L E E V L K T N R P L L 246

753 att att gca gat gat gtg gat ggt gaa gca ctt cca acc ctt gtc ttg aac aag att cgt ggt act ttc aat gtg 827
247 I I A D D V D G E A L P T L V L N K I R G T F N V 271

828 gtt gct gtc aaa ggc cca gga ttt ggt gat cgt cgt aaa gct atg ctt gaa gac att gct atc ttg aca ggt ggt 902
272 V A V K A P G F G D R K A M L E D I A I L T G G 296

903 aca gtg att aca gag gat cta gga ctt gaa tta aaa gat gct aca atg aca gcc ctt gga cag gct gct aag att 977
297 T V I T E D L G L E L K D A T M T A L G Q A A K I 321

978 aca gtt gat aaa gat agc aca gta att gtt gaa ggt tca gga agt tca gaa gct att gct aac cgt att gca ctg 1052
322 T V D K D S T V I V E G S G S S E A I A N R I A L 346

1053 att aaa tgc caa tta gaa aca aca act tct gac ttt gac cgt gaa aaa cta caa gaa cgt ttg ggc aaa tta gct 1127
347 I K S Q L E T T T S D F D R E K L Q E R L A K L A 371

1128 ggt ggt gta gct gtt atc aaa gta gga gct cca aca gag aca gct tta aaa gaa atg aaa ctt cgc att gag gat 1202
372 G G V A V I K V G A P T E T A L K E M K L R I E D 396

1203 gct cta aat gct aca cgt gca gcc gtt gaa gaa ggt atc gtt gct ggt ggt gga aca gca ctt att acc gtt att 1277
397 A L N A T R A A V E E G I V A G G G T A L I T V I 421

1278 gaa aaa gta gca gct ctt gag ctt gag gcc gat gat gct act gga cgt aac att gtg ctt cgt gct cta gaa gag 1352
422 E K V A A L E L E G D D A T G R N I V L R A L E E 446

1353 ctt gta cgt caa att gct tta aat gct ggc tac gaa gcc tcc gta gtt att gac aag ttg aaa aac agc cgt gca 1427
447 P V R Q I A L N A G Y E G S V V I D K L K N S P A 471

1428 gga aca gga ttt aat gct gca aca ggt gag tgg gtt gat atg att aaa aca gga atc att gac cgt gtc aaa gta 1502
472 G T G F N A A T G E W V D M I K T G I I D P V K V 496

1503 aca cga tca gcc ctt cca aat gca gct tct gta gct agt ctt att ttg aca aca gaa gca gtt gtt gct aat aaa 1577
497 T R S A L Q N A A S V A S L I L T T E A V V A N K 521

1578 cct gaa cca gct acc cca gcc cca gca atg cca gca ggt atg gat cca gga atg atg ggt ggc atg ggc gga tta 1652
522 P E P A T P A P A M P A G M D P G M N G G M G J 546

1653 gccgaattc 1661

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Figure 4

Sequencing strategy (scale : 1cm = approx. 100bp)

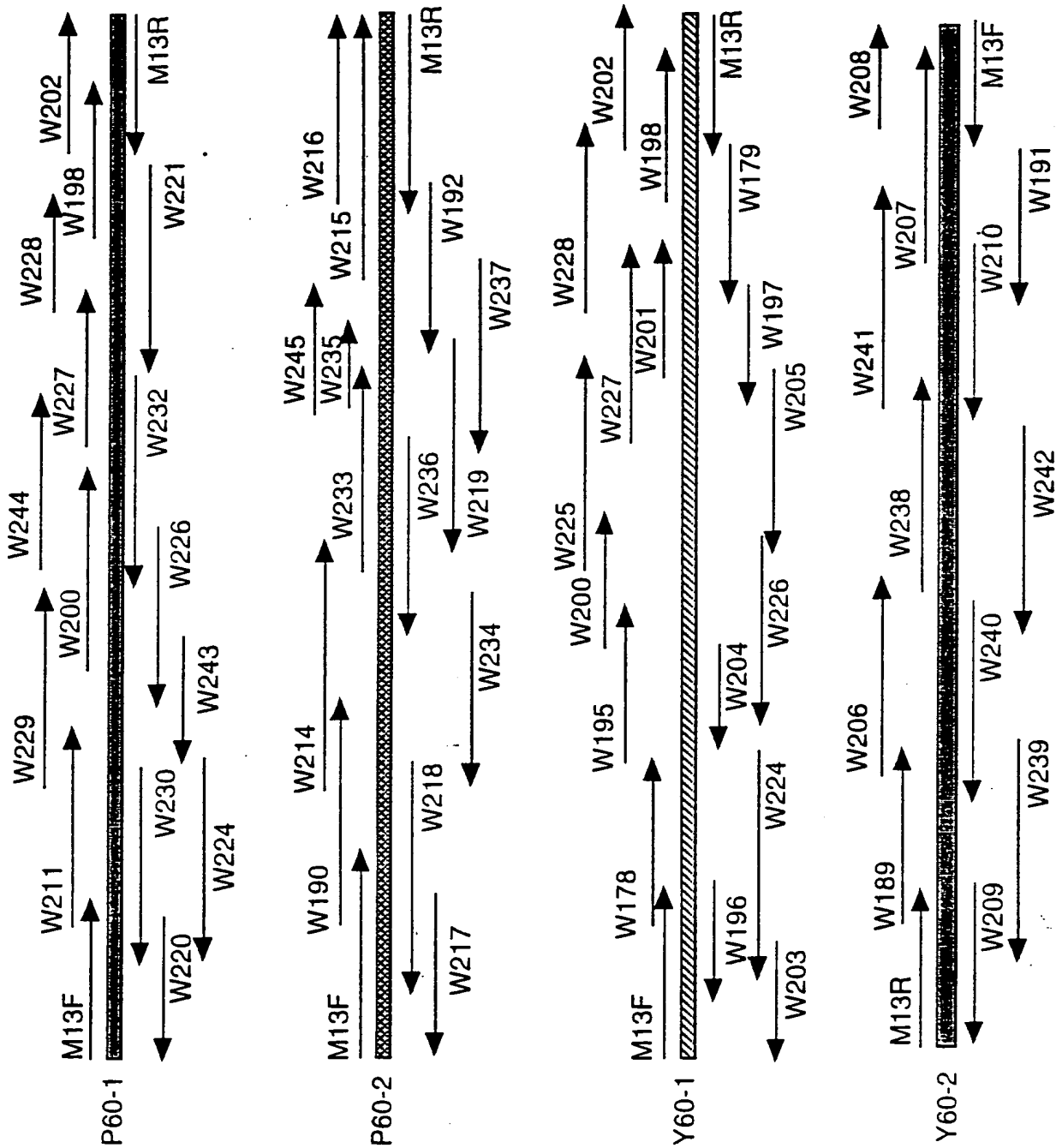


Figure 5

T7 expression construct f His-tagged *Streptococcus pneumoniae* hsp60-1
 PCR product starts at NdeI (58) site and ends at EcoRI site (1706)

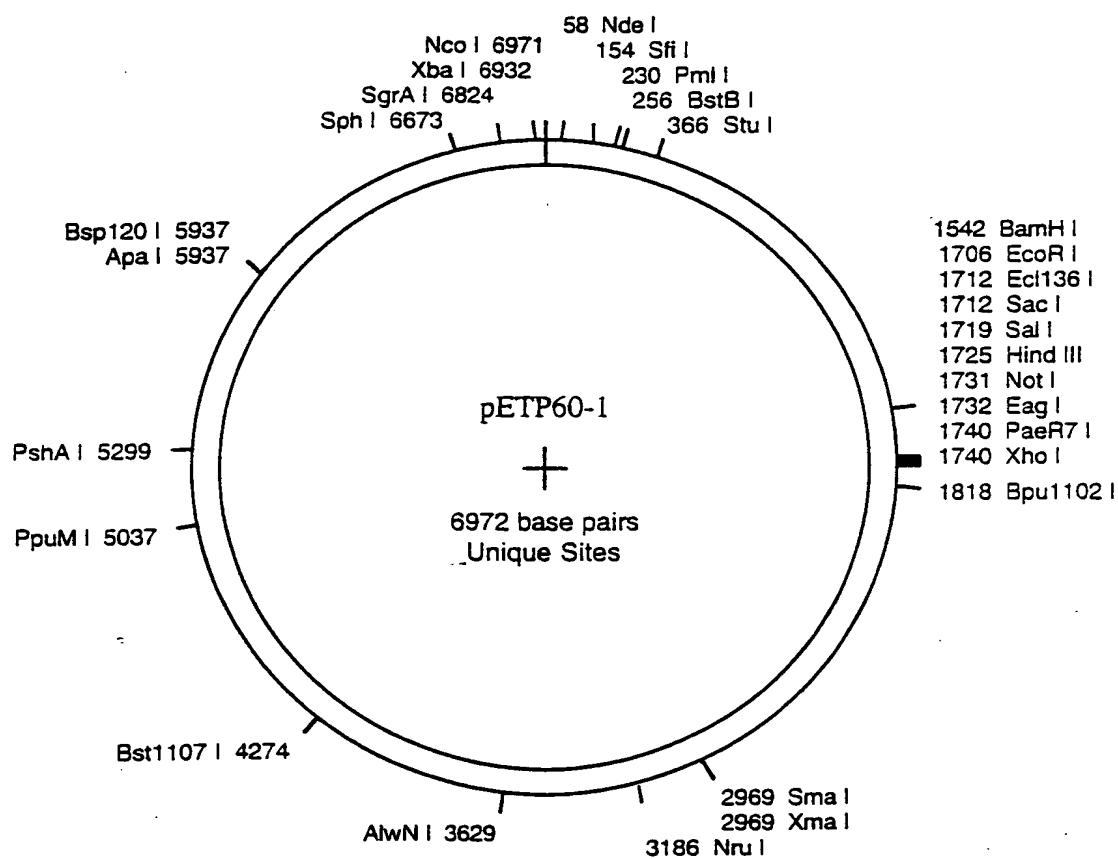


Figure 6

T7 expression construct of His-tagged *Streptococcus pneumoniae* hsp60-2
 PCR product starts at NdeI (58) site and ends at EcoRI site (1695)

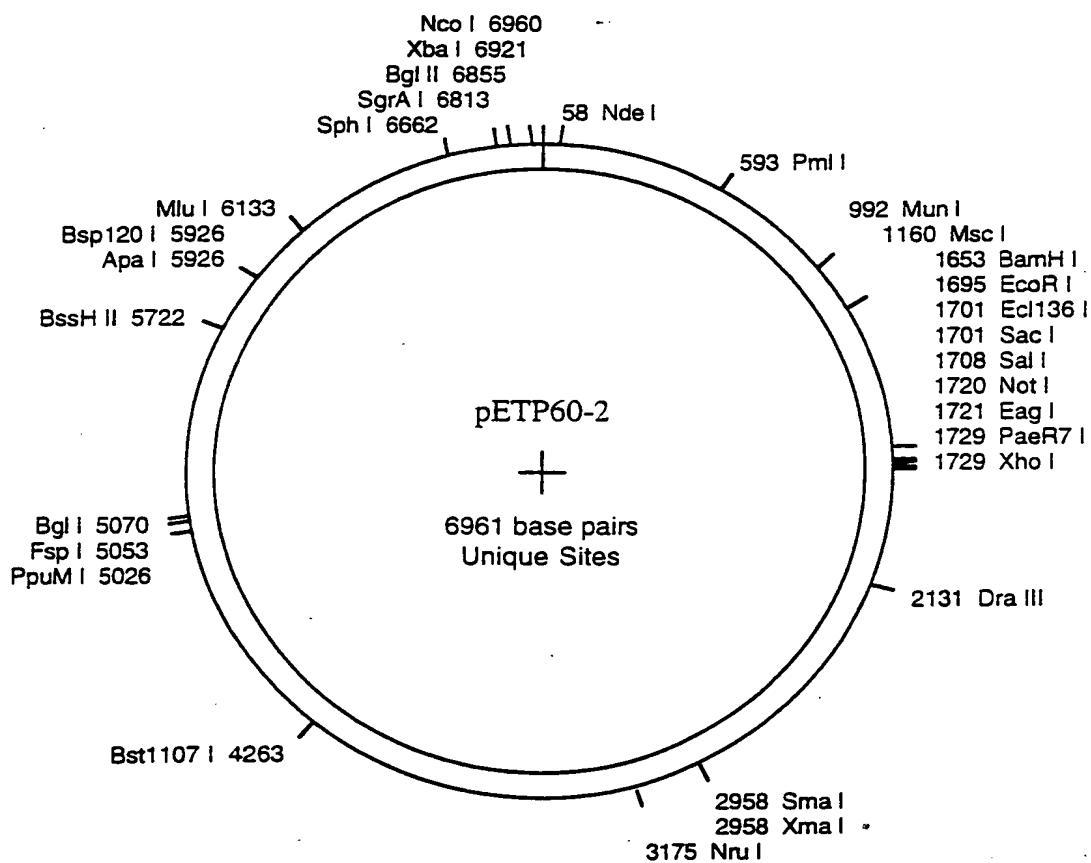


Figure 7

T7 expression construct of His-tagged *Streptococcus pyogenes* hsp60-1
 PCR product starts at NdeI (58) site and ends at EcoRI site (1703)

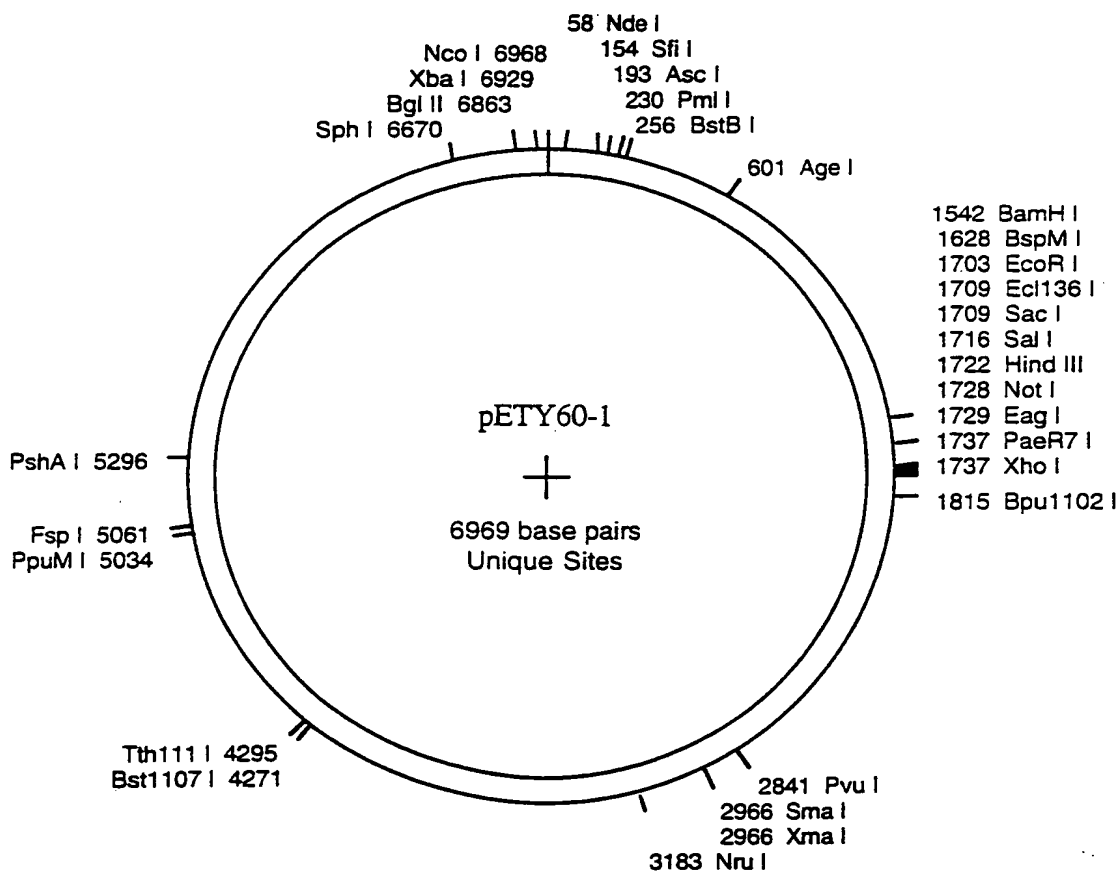


Figure 8

T7 expression construct of His-tagged *Streptococcus pyogenes* hsp60-2
 PCR product starts at NdeI (58) site and ends at EcoRI site (1702)

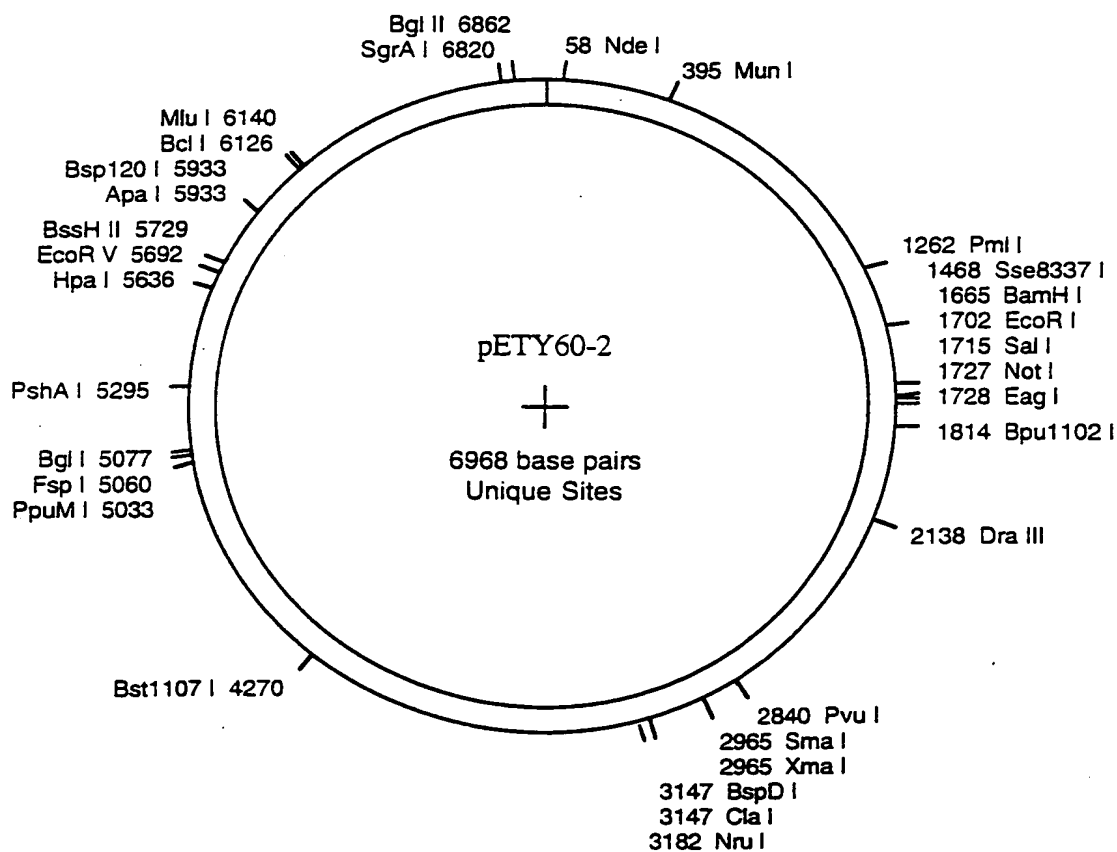


Figure 9

MA	10	20	30	40	50	60	70	80	90	100	110	120	130
S. pneumoniae hs MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
S. pyogenes hs MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
S. pneumoniae MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
S. pyogenes hs MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
B. subtilis gr MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
Clostridium h MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
Cowdria hsp60 MANM	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
Haemophilus h MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
L. pneumophila MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
M. avium hsp60 MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
M. bovis hsp60 MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
M. leprae groE HS	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
M. leprae hsp6 MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
M. tuberculosis MS	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
N. meningitidis MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
S. aureus hsp6 MV	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
Synechocystis MS	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
Synechocystis MS	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
Tsukamurella MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
S. pombe hsp60 M	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
S. cerevisiae M	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
P. falciparum M	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
Onchocerca hs MTNV	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
C. elegans hsp M	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
D. melanogaster H	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
human hsp60 M	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
Arabidopsis h M	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
maize hsp60 M	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA
RUBISCO chape	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA	MA

Figure 10A

	140	150	160	170	180	190	200	210	220	230	240	250	260
AGDGTITATVLAQAIUKBGLKRVAAAGANPMDLRGIDKAVDAVVEELKAIAPV--ETKEEIAQVATISANDEEIGE---AEAMKVKRGVITV---EEGKTLTELEVVEG-MQFDRGYLSPYFI													
S.pneumoniae	AGDGTITATVLAQSIITEGLKAVAAAGANPMDLRGIDKAVAAVVEELKALSVFC--SDSKAIAQVGTISANSDETGVK---AEAMDKVKGEGVITV---EDGTGLQDELDVVEG-MQFDRGYLSPYFI	205											
S.pyogenes hs	AGDGTITATVLAQAIITEGLKAVAAAGANPMDLRGIDKAVASVVEELKALSVFC--SDSKAIAQVGTISANSDETGVK---AEAMDKVKGEGVITV---EDGTGLQDELDVVEG-MQFDRGYLSPYFI	205											
S.pneumoniae	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITAVAAVVEELKKNVIVPV--ANKKEIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	203											
S.pyogenes hs	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	203											
B.subtilis gr	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	203											
Clostridium h	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	203											
Haemophilus hsp60	VGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	205											
L.pneumophila	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	205											
M.avium hsp60	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	204											
M.bovis hsp60	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	203											
M.leprae groE	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	203											
M.leprae hsp6	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	203											
M.tuberculosis	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	203											
N.meningitidis	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	203											
S.aureus hsp6	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	205											
Synechocystis	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	204											
Synechocystis	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	204											
Tsukamurella	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	203											
S.pombe hsp60	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	236											
S.cerevisiae	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	226											
P.falciparum	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	233											
Onchocerca hs	VGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	207											
C.elegans	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	220											
D.melanogaste	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	229											
human hsp60	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	229											
Arabidopsis h	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	235											
maize hsp60	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	238											
RUBISCO chape	AGDGTITATVLAQAIUREGINKVITAGANPIGIRGIEITATATAVVEELKAIAPV--SGKEAIAQVAVSS--RSEKVE---AEAMKVKRGVITV---EESRGMETELEVVEG-MQFDRGYLSPYFI	250											

Figure 10B

	270	280	290	300	310	320	330	340	350	360	370	380	390
S. pneumoniae	NKPTGAVELSPFILLADKKISNIREMLPVEAVA--	KAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
S. pyogenes	hs NKPETGAVELSPFILLADKKISNIREMLPVEAVA--	KAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
S. pneumoniae	TDSEKQAELEDPLILLTDKKISNIQDILLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
S. pneumoniae	TDSEKQAELEDPLILLTDKKISNIQDILLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
S. pyogenes	hs TDSEKQAELEDPLILLTDKKISNIQDILLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
B. subtilis	gr TDSEKQAELEDPLILLTDKKISNIQDILLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
Clostridium	h TDSEKQAELEDPLILLTDKKISNIQDILLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
Cowdria	hsp60 TDSEKQAELEDPLILLTDKKISNIQDILLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
Haemophilus	h NKPETGAVELSPFILLADKKISNIREMLPVEAVA--	KAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
L. pneumophila	hsp60 TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
M. avium	hsp60 TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
M. bovis	hsp60 TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
M. leprae	groE TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
M. tuberculosis	hsp60 TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
N. meningitidis	hsp60 TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
S. aureus	hsp60 TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
Synechocystis	hsp60 TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
Tsukamurella	hsp60 TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
S. pombe	hsp60 TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
S. cerevisiae	hsp60 TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
P. falciparum	hsp60 TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
Onchocerca	hsp60 TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
C. elegans	hsp60 TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
D. melanogaster	hsp60 TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
human	hsp60 TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
Arabidopsis	hsp60 TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
maize	hsp60 TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							
RUBISCO	chape TDSEKQAELEDPLILLTDKKISNIREMLPVEEVA--	OAGKPLIIIAEDVVEGEALATLVNTHRGIVKVA	PGFGRKAMQDIAITLTCGTVISEE--	IGMELEKATLED--	LGQAKRVVINKDITTT	331							

Figure 10C

IVDGAGD--AAIAGRVQIRSQIEEST--SDYDKEKLOERLAKLAGGVAVIKVGAATEVELKERKDRVEDALANTRAABEGIVPGGVALRAAPALDKLKE--NGDEATGNIVILRALERPLRQIAE
 400 410 420 430 440 450 460 470 480 490 500 510 520
 S. pneumoniae IIDGVGD--EAAIQRVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 456
 S. pyogenes hsp IIDGVGD--EAAIQRVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 456
 S. pneumoniae IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 453
 S. pyogenes hsp IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 453
 B. subtilis gr IVEBAGE--TUKISARVQIRQIEEAT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 453
 Clostridium h IVEBAGN--SEENIKRINQIKQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 453
 Cowdria hsp60 IIDGVGD--EAAIQRVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 454
 Haemophilus h IIDGVGD--EAAIQRVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 458
 L. pneumophila IIDGVGD--EAAIQRVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 455
 M. avium hsp60 IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 455
 M. bovis hsp60 IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 453
 M. leprae groE IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 453
 M. leprae hsp60 IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 453
 M. tuberculosis IIDGVGD--EAAIQRVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 456
 M. meningitidis IIDGVGD--EAAIQRVQIRQIEEAT--SDYDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 456
 S. aureus hsp60 IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 456
 Synechocystis IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 454
 Synechocystis IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 454
 Tsukamurella IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 458
 S. pombe hsp60 IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 452
 S. cerevisiae IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 488
 P. falciparum IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 478
 Onchocerca hsp IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 483
 C. elegans hsp IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 459
 D. melanogaster IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 472
 human hsp60 IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 481
 Arabidopsis hsp60 IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 486
 maize hsp60 IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 489
 RUBISCO chape IVEBAGN--FENAIHRVAVIKSQIEETT--SEFDREKLOERLAKLAGGVAVIKVGAATEVEHEKKEKARVEDALJHATRAAABEGVWAGGVALIRVASKIAGIKQ--NEDQNVGKVALRAMESPLRQIVL 503

NAGLEGSV-VVEKVN---SEAG-GYNAATGEVDMIAAGIIDPTKVTSALQNAASVASLMTTTEAVVDKPEKAPAG-MFGM---MCGMCGMGM---M-620

S. pneumoniae NCGFEPSV-VNTVKA---GDGNGYGYNAATEEYGNMIDMGILDFPKVTSALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG-620

S. pyogenes hs NAGEEPSV-VNTVKA---GEGNGYGYNAATEEYGNMIDMGILDFPKVTSALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG-620

S. pneumoniae NAFEGSI-VIDRLKN---ABLGIFGNAATGEWMNIDQGIIDPKVTSALQNAASVASLITTEAVANKPEFVAPAPA-M---DPSMCMGKGG

S. pyogenes hs NAGYEGSV-VIDRLKN---SPAGTGNAATGEWMIKTIGIDPKVTSALQNAASVASLITTEAVANKPEFVAPAPA-M---DPSMCMGKGG

B. subtilis gr NAGLEGSV-VIERLKN---BEIGVGFNAAATGEWMNIEKGIIDPKVTSALQNAASVASLITTEAVANKPEFVAPAPA-MPGAMDPCMGCMGKG

Clostridium h NAGLEGSV-IIEKLVN---SDAGVGFDALRGEWMNIEKGIIDPKVTSALQNAASVASLITTEAVANKPEFVAPAPA-M---DPSMCMGKGG

Cowdria hsp60 NAGSENAFCVTAHLKQNDKELI---FNVDVTFNAAFTSGVIDPLKVVRLAFDFVSLAAVFTWLNALVDIPSKDDNSAAGNGMGCMGKG-620

Haemophilus h NAGEEASV-IASAVKN---BKGNFGYNAATGEQGMNIAAGILDFPKVTSALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

L. pneumophila NAGEEASV-VNKNVE---HKGNGYGYNAATEEYGNMIDMGILDFPKVTSALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

M. avium hsp60 NCGLEFV-VAEKVRN---SPAGTGLNAAATGEVEDLLKAGIADVPKVTSTRALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

M. bovis hsp60 NSGLEFV-VAEKVRN---LPAGHGLNAAATGEVEDLLKAGIADVPKVTSTRALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

M. leprae groE NAGLDAN-VVDKVG---LPAGHGLNASTGVEDLLKAGIADVPKVTSTRALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

M. leprae hsp6 NSMGFV-VAEKVRN---LSVGHGLNAAATGEVEDLLKAGIADVPKVTSTRALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

M. tuberculosis NAGLDGV-VVKVSE---LPAGHGLNASTGVEDLLKAGIADVPKVTSTRALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

N. meningitidis NAGEEPSV-VNKNVE---HKGNGYGYNAATEEYGNMIDMGILDFPKVTSALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

S. aureus hsp6 NAGLEGSV-IIEKLVN---KEFNGYGYNAATGEQGMNIAAGILDFPKVTSALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

Synechocystis NAGQNAV-ISEKVE---KEFNGYGYNAATGEQGMNIAAGILDFPKVTSALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

Synechocystis NAGLEGSV-IIEKLVN---KEFNGYGYNAATGEQGMNIAAGILDFPKVTSALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

Tsakumarella NAGLEGSV-IIEKLVN---ATNGQYNAVITCKIEDLLKAGIADVPKVTSTRALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

S. pombe hsp60 NAGLEGNL-IVGKLKELGKEFNIGDIADKDFVRLNEIGVLDPLKVVRLAFDFVSLAAVFTWLNALVDIPSKDDNSAAGNGMGCMGKG-620

S. cerevisiae NAGEGSV-IIGKLDIEYGDPAKGYDASKSEYDMATGIDPEKVVSRGLVDASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

P. falciparum NAGHIEGSV-VAGNLIKDNKNSI---GFNAQEGKYDMNIESGIIIDPKVTSALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

Onchocerca hs NAGLEGSV-IIDYLIKQNKELI---NVNEAMSYNAAFAAGVIDPKVTRALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

C. elegans hsp NAGLEPSS-IIDYLIKQNKELI---NVNEAMSYNAAFAAGVIDPKVTRALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

D. melanogaster NAGVGM-VAKVQNG-DY---GYDA-KGEYGNLIEKGIIDPKVTRALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

human hsp60 NAGVGSV-IIEKLVN-QSSEV---GYDAMAGDFVNNVEKGIIDPKVTRALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

Arabidopsis h NAGVGSV-IIEKLVN-QSSEV---GYDAMAGDFVNNVEKGIIDPKVTRALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

maize hsp60 NAGVGSV-IIEKLVN-QSSEV---GYDAMAGDFVNNVEKGIIDPKVTRALQNAASVAGLMITTECMVTDLPKGDAPDLG-AAG---MGCMCGG

RUBISCO chape NAGIEGSV-VVEKVN---GEMEVGYNAATGEVDMIAAGIIDPTKVTSALQNAASVAGLMITTEAVVDKPEKAPAG-MFGM---MCGMCGMGM---M-620

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Current Chromatogram(s)

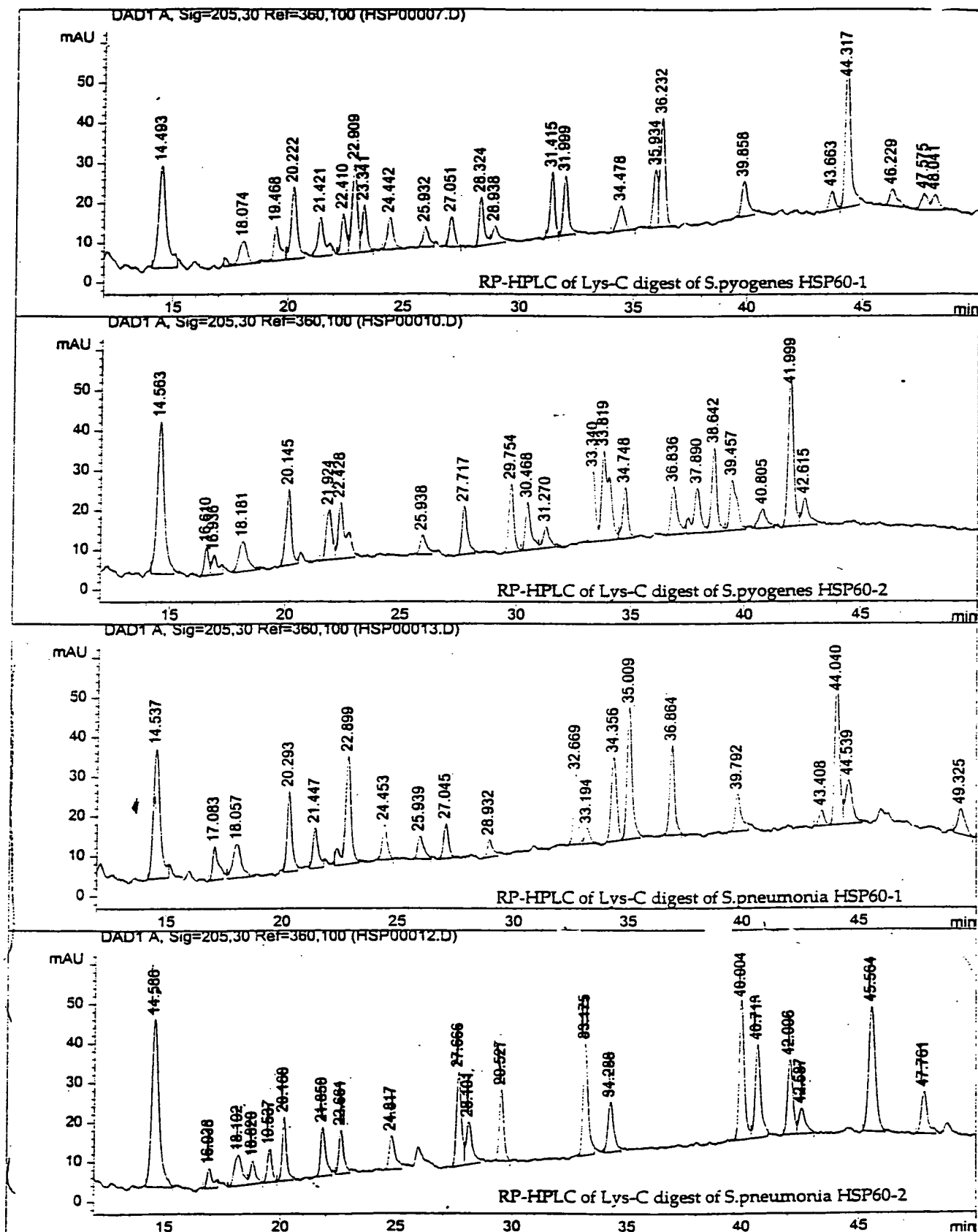


Figure 11